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EC-11775.DNA 25: ACACCGGTCAACATTGAGGAAGAGCTGAAGAGCTCCTATCTGGATTATGCGATGTCGGTC  
 CF-8090.DNA .....  
 EA-13048.DNA .....G.....A.....G.....  
 ECL13047.DNA .....T.....C.....C.....  
 KO-13182.DNA .....  
 KP-13883.DNA .....T...A...T.....  
 PS-29914.DNA .....T.C.A....A.C.A..T.G..T.....C..T  
 SM-13880.DNA .....A....C..A..C...T...A.A..G.....C.....C..T  
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EC-11775.DNA 85: ATTGTTGGCCGTGCGCTGCCAGATGTCCGAGATGGCCTGAAGCCCGGTACACCGTCGCGTA  
 CF-8090.DNA .....C.....T.....  
 EA-13048.DNA .....G.....  
 ECL13047.DNA .....G.C....C.....  
 KO-13182.DNA .....G.....  
 KP-13883.DNA .....G.....  
 PS-29914.DNA .....C.G..C....T.....T.....A.....A.....CA.A..  
 SM-13880.DNA .....C..A....C.....T..T....A.....T....C....T  
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EC-11775.DNA 145: CTTTACGCCATGAACGTACTAGGCAATGACTGGAACAAAGCCTATAAAAAATCTGCCCGT  
 CF-8090.DNA .....T.G....C.....T.....  
 EA-13048.DNA ..A.....T.G.....A.....  
 ECL13047.DNA ..A.....T.G.....T.....C.....  
 KO-13182.DNA ..A.....T.G.....A.....  
 KP-13883.DNA .....T.G.....  
 PS-29914.DNA ..G.TT..G....T..T.G..A....T....T..C.....  
 SM-13880.DNA ..G....G....G....T.G..T..C.....T..C.A..C..G....G.....  
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EC-11775.DNA 205: GTCGTTGGTGACGTAATCGGTAAATACCATCCCCATGGTGACTCGCGGTTTATGACACG  
 CF-8090.DNA .....C..T.....TA.C..C....C....C  
 EA-13048.DNA .....C.....C.G.....TA.C..C....C  
 ECL13047.DNA .....T..C....G..C....C  
 KO-13182.DNA .....G.....C.....C..T.....TA.T..C..A..C....C  
 KP-13883.DNA .....C.G..C..C....C....A..C....C  
 PS-29914.DNA A.A..C..G....T.....A.....TAGC..T.....G..A  
 SM-13880.DNA .....C..G....G.....T..C..G..C....AGC.....C....T  
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EC-11775.DNA 265: ATCGTCCGTATGGCGCAGCCATTCTCGCTGCGTTACATGCTGGTAGACGGTCAGGGTAAC  
 CF-8090.DNA ..T..T.....CT.....T.....  
 EA-13048.DNA .....A.....G....CT.....T.....C..T..C.....  
 ECL13047.DNA .....T.....T.....T.....  
 KO-13182.DNA ..T..A.....C.....T..C.....  
 KP-13883.DNA .....G.....G.....G....C.....  
 PS-29914.DNA .....T..C.T..T....T..T..TA.....T.....T.....G..  
 SM-13880.DNA .....G.....T....G..T..A....C.....G.....  
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Fig - 1A

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EC-11775.DNA 325: TTCGGTTCCATCGACGGCGACTCTCGCGCGGCAATGCGTTATACGGAAATCCGTCTGGCG  
CF-8090.DNA ..T....TG...T.....C..A....G.....A..T..  
EA-13048.DNA ..T....TG...T.....C..T..A..G.....A..T..  
ECL13047.DNA ..T....T.....C..C.....A..T..  
KO-13182.DNA ..T....GG.....C..C..A..G.....A..T..  
KP-13883.DNA ..T.....C..C.....G.....C....T.....  
PS-29914.DNA ..T....AG.T....A..T..C..A..T.....A.....  
SM-13880.DNA .....G.....C.....G.....C..G.G..CA..T.C  
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EC-11775.DNA 385: AAAATTGCCCATGAACTGATGGCTGATCTCGAAAAAGAGACGGTCGATTTCGTTGATAAC  
CF-8090.DNA .....C.....G.....C..G.....A.....T.....C.....  
EA-13048.DNA ..G..C..T.....G.....C.....T.....C..C..  
ECL13047.DNA .....G.....C..C..G.....T.....  
KO-13182.DNA ..G..C.....C..C.....G.....C.....  
KP-13883.DNA .....C..T....G.....C....T.....C..C..  
PS-29914.DNA .....A..T.A..G....T.....C..T.....CCCA..  
SM-13880.DNA ..G.....T..C.....T...G.....A..C.....GCC...  
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EC-11775.DNA 445: TATGACGGTACGGAAAAAATTCGGGACGTCATGCCAACCAAAATTCCTAACCTGCTGGTG  
CF-8090.DNA ..C.....C..C...C.....T.....G.....  
EA-13048.DNA .....C.....G....C..T.....G..A....C.....  
ECL13047.DNA ..C..T..C.....T.....G..G..C.....  
KO-13182.DNA .....C.....G....C..T....T....G.....C..G.....A..C  
KP-13883.DNA .....GCGT.....G.....  
PS-29914.DNA ....T....A..GC...C..T..A..T....T..G....C.....AT...T  
SM-13880.DNA ....T..C..C..GC.G..C....C.....G....G..C..G.....C  
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EC-11775.DNA 505: AACGGTTCTTCCGGTATCGCCGTAGGTATGGCAACCAACATCCCGCCGCACAACCTGACG  
CF-8090.DNA .....G.....G.....T.....T.....  
EA-13048.DNA .....G.....G.....T.....A..C..C  
ECL13047.DNA .....G.....G.....G.....T.....C  
KO-13182.DNA .....G.....G.....G.....C.....A..T.....  
KP-13883.DNA ....CG.C....G.....G.....C.....A..T.....  
PS-29914.DNA ..T....G..A....T..T..T..G.....G....T..T..A.....AGG.  
SM-13880.DNA ....C..G..G..C.....G..C....T....T..T.....G..  
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EC-11775.DNA 565: GAAGTCATCAACGGTTGTCTGGCGTATATCGATGATGAAGACATCAGCA  
CF-8090.DNA .....G.....C.....A....T..C.....  
EA-13048.DNA ....T.....C..C....A..CG.T...A.C.....  
ECL13047.DNA ....G.....C..C.....C.....C.....  
KO-13182.DNA ....G.....C.....C..CG.T..AA.C.....  
KP-13883.DNA ....G..T....C.....G.T..C.....  
PS-29914.DNA ....G...G....C..T..T....A.....T..T....  
SM-13880.DNA .....G.....C..C....C.....C.....A.....  
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Fig - 1B

### rdDNA Sequence Similarity of the QRDR in Enterobacteriaceae

	199	S83	258
<i>E. coli</i> **	GCCCGTGTGGTGACGTAATCGGTAATAACCATCCCATGGTGACTCGGGCGGTTTAT		
<i>C. freundii</i>	.....	.....C.T.....TA.C.C.....C	
<i>E. aerogenes</i>	.....C.....	.....C.G.....TA.C.C.....	
<i>E. cloacae</i>	.....	.....T.C.....G.C	
<i>K. oxytoca</i>	.....G.....C.....	.....T.....TA.T.C.A.C	
<i>K. pneumoniae</i>	.....	.....C.G.C.C.....A.C	
<i>P. stuartii</i>	.....A.A.C.G.....T.....	.....TAGC.T.....	
<i>S. marcescens</i>	.....C.G.....G.....T.C.G.C.....AGC.....C		
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[illegible]

\* Yoshida et al., 1990. Antimicrob. Agents Chemother. 34:1271.  
\* Swanberg and Wang, 1987. J. Mol. Biol. 197:729.

Similarity of the Amino Acid Sequences of the QRDR  
of Enterobacteriaceae

	67	83	87	106
<i>E. coli</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM
<i>C. freundii</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM
<i>E. aerogenes</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM
<i>E. cloacae</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM
<i>K. oxytoca</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM
<i>K. pneumoniae</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM
<i>P. stuartii</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM
<i>S. marcescens</i>	ARVVG	VDVIGKYHPHGDS	AVYDTIV	RM

Fig - 3

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Strain	MIC ( $\mu\text{g/ml}$ ) <sup>1</sup>			Amino acid change <sup>2</sup>		
	CIP	OFLX	SPAR	81	GyrA 83	87 (codon)
<b><i>C. freundii</i></b>						
ATCC 8090	$\leq 0.12$	$\leq 0.25$	$\leq 0.008$	Gly (GGT)	Thr (ACC)	Asp (GAC)
Cf 7377	2	8	>2	-	Ile (ATC)	-
Cf 0759	2	8	>2	-	Ile (ATC)	-
Cf 9085	4	8	2	-	Ile (ATC)	-
Cf 9417	8	8	>2	-	Ile (ATC)	-
Cf 1958	$\geq 16$	$\geq 16$	>2	-	Ile (ATC)	Gly (GGC)
Cf 5757	$\geq 16$	$\geq 16$	>2	-	Ile (ATC)	Gly (GGC)
Cf 9023	$\geq 16$	$\geq 16$	>2	-	Ile (ATC)	-
<b><i>E. aerogenes</i></b>						
ATCC 13048	0.5	1	0.25	Gly (GGT)	Thr (ACC)	Asp (GAC)
Ea 1747	$\leq 0.12$	<0.25	0.06	-	-	-
Ea 2786	2	4	2	-	Ile (ATC)	-
Ea 9032	4	4	2	-	Ile (ATC)	-
Ea 5593	8	8	>2	-	Ile (ATC)	-
Ea 9433	8	$\geq 16$	>2	-	Ile (ATC)	-
Ea 3521	8	$\geq 16$	>2	-	Ile (ATC)	-
Ea 5590	8	$\geq 16$	>2	-	Ile (ATC)	-
Ea 2775	$\geq 16$	32	>2	-	Ile (ATC)	-
<b><i>E. cloacae</i></b>						
ATCC 13047	$\leq 0.12$	$\leq 0.25$	0.03	Gly (GGT)	Ser (TCC)	Asp (GAC)
Ecl 1700	$\leq 0.12$	<0.25	0.06	-	-	-
Ecl 1524	0.25	0.5	0.12	-	-	Asn (AAC)
Ecl 1963	2	4	2	-	Phe (TTC)	-
Ecl 1286	2	4	1	-	Tyr (TAC)	-
Ecl 3529	4	8	>2	-	Thr (ACC)	-
Ecl 1544	8	8	>2	-	Tyr (TAC)	-
Ecl 1627	8	$\geq 16$	>2	-	Tyr (TAC)	-
Ecl 9028	$\geq 16$	8	>2	-	Ile (ATC)	-
Ecl 1224	$\geq 16$	8	>2	-	Phe (TTC)	Asn (AAC)
Ecl 1251	$\geq 16$	$\geq 16$	>2	-	Ile (ATC)	-
Ecl 63	$\geq 16$	$\geq 16$	>2	-	Phe (TTC)	-
Ecl 105	$\geq 16$	$\geq 16$	>2	-	Phe (TTC)	-
Ecl 1783	$\geq 16$	$\geq 16$	>2	-	Tyr (TAC)	-
Ecl 9030	$\geq 16$	$\geq 16$	>2	-	Tyr (TAC)	-
Ecl 9031	$\geq 16$	>32	>2	-	Ile (ATC)	-
<b><i>E. coli</i></b>						
ATCC 11775	$\leq 0.12$	$\leq 0.25$	0.03	Gly (GGT)	Ser (TCG)	Asp (GAC)
Ec 748	$\leq 0.12$	$\leq 0.25$	0.03	-	-	-
Ec 3535	1	2	2	-	Leu (TTG)	-
Ec 5524	2	8	2	-	Leu (TTG)	-
Ec 9419	$\geq 16$	32	>2	-	Leu (TTG)	Gly (GGA)
Ec 9421	$\geq 16$	32	>2	-	Leu (TTG)	Tyr (TAC)
Ec 9425	$\geq 16$	>32	>2	-	Leu (TTG)	Asn (AAC)


 4A

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Strain	MIC ( $\mu\text{g/ml}$ )			Amino acid change		
	CIP	OFLX	SPAR	81	GyrA 83	87 (codon)
<b><i>K. pneumoniae</i></b>						
ATCC 13883	0.5	$\leq 0.25$	0.06	Gly (GGC)	Ser (TCC)	Asp (GAC)
Kp 570	$\leq 0.12$	$\leq 0.25$	0.06	-	-	-
Kp 1961	$\leq 0.12$	$\leq 0.25$	0.03	-	-	-
Kp 2778	$\leq 0.12$	$\leq 0.25$	0.03	-	-	-
Kp 2790	$\leq 0.12$	$\leq 0.25$	0.03	-	-	-
Kp 1361	1	2	0.5	-	Phe (TTC)	-
Kp 1362	1	2	1	-	Phe (TTC)	-
Kp 1177	4	$\geq 16$	$> 2$	-	Phe (TTC)	-
Kp 682	$\geq 16$	$\geq 16$	$> 2$	-	Phe (TTC)	-
Kp 1768	$\geq 16$	32	$> 2$	-	Tyr (TAC)	-
Kp 1775	$\geq 16$	$> 32$	$> 2$	-	Phe (TTC)	Gly (GGC)
Kp 1565	$\geq 16$	$> 32$	$> 2$	-	Tyr (TAC)	Asn (AAC)
<b><i>K. oxytoca</i></b>						
ATCC 13182	$\leq 0.12$	$\leq 0.25$	0.12	Gly (GGT)	Thr (ACT)	Asp (GAC)
Ko 702	$\leq 0.12$	$\leq 0.25$	0.03	-	-	-
Ko 2538	$\leq 0.12$	$\leq 0.25$	0.06	-	-	-
Ko 2110	$\leq 0.12$	$\leq 0.25$	0.06	-	-	-
Ko 1199	$\leq 0.12$	$\leq 0.25$	0.06	-	-	-
Ko 57	0.5	0.05	0.25	-	Ile (ATT)	-
Ko 1577	4	4	2	-	Ile (ATT)	-
Ko 1817	8	$\geq 16$	$> 2$	-	Ile (ATT)	-
Ko 466	$\geq 16$	8	$> 2$	-	Ile (ATT)	-
Ko 32	$\geq 16$	$\geq 16$	$> 2$	-	Ile (ATT)	-
Ko 1578	$\geq 16$	$\geq 16$	$> 2$	-	Ile (ATT)	-
Ko 1612	$\geq 16$	$\geq 16$	$> 2$	-	Ile (ATT)	-
Ko 2777	$\geq 16$	$> 32$	$> 2$	-	Ile (ATT)	-
<b><i>P. stuartii</i></b>						
ATCC 29914	$\leq 0.12$	$\leq 0.25$	$\leq 0.12$	Gly (GGT)	Ser (AGC)	Glu (GAG)
Ps 1571	0.25	1	0.5	-	-	-
Ps 1284	2	4	2	-	Arg (CGC)	-
Ps 2469	8	$\geq 16$	$> 2$	-	Ile (ATC)	-
Ps 2783	$\geq 16$	$\geq 16$	2	-	Arg (AGG)	-
Ps 9428	$\geq 16$	$\geq 16$	$> 2$	-	Ile (ATC)	-
Ps 7375	$\geq 16$	32	$> 2$	-	Ile (ATC)	-
Ps 2468	$\geq 16$	32	$> 2$	-	Ile (ATC)	-
Ps 1773	$\geq 16$	$> 32$	$> 2$	-	Arg (AGG)	-
<b><i>S. marcescens</i></b>						
ATCC 13880	0.5	1	1	Gly (GGT)	Ser (AGC)	Asp (GAC)
Sm 1714	0.25	1	1	-	-	-
Sm 9745	2	4	2	-	Ile (ATC)	-
Sm 1221	4	8	$> 2$	Cys (TGT)	-	-
Sm 1969	4	$\geq 16$	$> 2$	-	-	Asn (AAC)
Sm 1570	8	8	$> 2$	Cys (TGT)	-	-
Sm 5591	8	$\geq 16$	$> 2$	-	Arg (AGA)	-
Sm 1568	$\geq 16$	$\geq 16$	$> 2$	-	Arg (CGC)	-

<sup>1</sup> CIP, ciprofloxacin; OFLX, ofloxacin; SPAR, sparfloxacin<sup>2</sup> -, identical to the ATCC type strain

4B